

ACGCAACTTCGGGCCAGGGGTCCGCCCAAGGGGTCCGAAGAGCCTTGAACCGGCCCCGGCTCCTTGACCTTGCTTGT [SEQ ID NO:1]

GGGGCGAAGGACTGCCCCCTGGGCGCTGGGTCCGGGTGTGCCCCCTTCTCACTTGAAGACATGCAGGCCCTGACTCTCCG

CACACTTGGCCCGCCAGCGACGTCACCCAGCACCTACGAACTAGTCCCGGGAGCTGGGCAAAGGCACCTACGGGAG

	M A L K F V N K S K	10 [SEQ ID NO:2]
GTTGATCTGGTGGTCTACAAGGGCACAGGCACAAA	ATG GCA CTG AAG TTT GTG AAC AAG AGC AAA	30

↑ SEQ ID NO: 3 →

T K L K N F L R E V S I T N S L S S S P 30
ACC AGG CTG AAG AAC TTC CTA CGG GAG GTG AGC ATC ACC AAC AGC CTC TCC TCC AGC CCC 90

F I I K V F D V V F E T E D C Y V F A Q 50
TTC ATC ATC AAG GTC TTT GAC GTG GTC TTT GAG ACA GAG GAC TGC TAC GTC TTT GCC CAG 150

E Y A P A G D L F D I I P P Q V G L P E 70
GAG TAC GCA CCT GCT GGG GAC CTG TTT GAC ATC ATC CCT CCC CAG GTG GGG CTC CCT GAG 210

D T V K R C V Q Q L G L A L D F M H G R 90
CAC ACG GTG AAG CGC TGT GTG CAG CAG CTG GGC CTG GCG CTG GAC TTC ATG CAC GGG CGG 270

Q L V H R D I K P E N V L L F D R E C R 110
CAG CTG GTG CAC CGC GAC ATC AAG CCC GAG AAC GTG CTG CTG TTC GAC CGC GAG TGC CGC 330

R V K L A D F G M T R R V G C R V K R V 130
CGC GTA AAG CTG GCC GAC TTC GGC ATG ACG CGC CGC GTG GGC TGC CGC GTC AAG CGC GTG 390

S G T I P Y T A P E V C Q A G R A D G L 150
AGC GGC ACC ATC CCT TAC ACG GCG CCT GAG GTG TGC CAG GCG GGC CGC GCC GAC GGG CTG 450

A V D T G V D V W A F G V L I F C V L T 170
GCG GTG GAC ACG GGC GTG GAC GTG TGG GCC TTC GGC GTG CTC ATC TTC TGC GTG CTC ACC 510

G N F P W E A A S G A D A F F E E F V R 190
GGC AAC TTC CCG TGG GAG GCG GCG TCG GGC GCC GAC GCC TTC TTC GAG GAG TTC GTG CGC 570

W Q R G R L P G L P S Q W R R F T E P A 210
TGG CAG CGG GGC CGC CTG CCG GGG CTG CCT TCG CAG TGG CGC CGC TTC ACC GAG CCC GCG 630

FIG. 1A

2/21

L R M F Q R L L A L E P E R R G P A K E 230
CTG CGC ATG TTC CAG CGC TTA CTG GCC CTG GAG CCC GAG CGC CGC GGC CCA GCC AAG GAG 690

V F R F L K H E L T S E L R R R P S H R 250
GTG TTC CGC TTC CTC AAG CAC GAG CTC ACG TCC GAG CTG CGC CGC CGG CCC TCG CAC CGC 750

A R K P P G D R P P A A G P L R L E A P 270
GCG CGC AAG CCC CCC GGG GAC CGC CCG CCC GCC GCC GGG CCA CTG CGC CTC GAG GCG CCT 810

G P L K R T V L T E S G S G S R P A P P 290
GGG CCG CTC AAG CGG ACG GTG CTG ACC GAG AGC GGC AGC GGC TCC CGG CCC GCG CCC CCC 870

A V G S V P L P V P V P V P V P V P V P 310
GCC GTC GGG TCG GTG CCC TTG CCC GTG CCG GTG CCG GTG CCA GTG CCC GTG CCG GTG CCT 930

V P E P G L A P Q G P P G R T D G R A D 330
GTG CCC GAG CCC GGC CTA GCT CCC CAG GGG CCC CCC GGC CGG ACC GAC GGC CGC GCG GAC 990

K S K G Q V V L A T A I E I C V * 347
AAG AGC AAA GGG CAG GTG GTG CTG GCC ACG GCC ATC GAG ATC TGC GTC TGA 1041

← SEQ ID NO:3↑

GTCCGCTCCGCGCCCTCGGACCCGGGAGCAGCCCGGGCCCGCCCGAGCCGGTGCCCGGTGCGGCGGTAGGGAATGGA
GCCACCTCGCGCGGGGCGAGGGGCGCAGCGGTAGACTAGGCAGGACGCGCCCGGCACCTGGTCCGTCCCCGGCGGGC
TGGTGAGGGGGCCACCAAGACCCCTAGCGCGGCTGGTGAGCGGGGCTTGGCCAGAGGAGCAAGCCGCACAGACC
CGAGAATTGCGAGGCCACCACACAACACACACACATACACACACACACACACGCGCAGGAGCAAGGGAGC
TTTCGGGCCACACTCCAGACGCTCCCTGAGCCCTGGAACCCGGACTCGTTGCTCCTGGCCTTCCATACCCCTGGCA
GATCATCTCGCGTCCACCCAGATCCCTCCTCCTCGCCATCCATTCTGCCCCCTCCCCACCCCTGGGTACAGAAAG
GGACTGAAGTGTGGGCAGAGAGGGGCTTAAGGCCCTGGGCACAGGCTGGGATCAGGGCAGTGAGCGAAGGGCAGCT
GTGTCCTGCCCTTCTCTGAGGCTGGAGGGGAGAGGCCAAGCCCTTGAAAAATGTAGCAAATGCTGGRWKTCGCA

FIG. 1B

3/21

TAAGTGGGTGTATGTGCGGGACAGGCCCCGAGAAGCTAGTACTCCTGCACACCCCATTCACAAATGAAATCACAGC
CCAGGAGGGAGGGTAGCTTGGCACTGGCTGAGAAATAGAGCTCTCTCCCGCCCTCCCTAACCACAAGGGATTGTC
CTGACAACCTTGTGGGATAGAAGGGCTCACAGGGCAGGGGTCTCAGCTGCCCCATCCTTAGGGCAGGGAGTTAGTGT
GGAGCCGAGAGCAGGTCCCAGCTCCCCCTGCCAGCCGCACTGTCCAGGCCAGGGACCTCTGCCGGGTCTCCAGCC
CTTGCCACACAGCCTAGACCTAGTAGCTGGGCTTCCAGCAGGTGGCGAGCTGGTTCGTGCTGAAATTTCTCTGGGT
TTCTTGGGGTCAAACATGCCAACCTCCAAGACCCATCCTCAGTCTCCACTTTTCTGGCGCTGGAGTGTGCAGGGCG
TAGGACCTGCATGTGTGGGTGTGAGAATGGGGCCGGTGGACACCAGGGGCGAGTGTGTGACTAGGTGTGTGCACA
TGTGTAGGGTGCAGACGCATGGGTGCCATCCTTTGCTTCAATGACTGTGCGTCCAGACCCAAAAAGCGGCCCCC
ACCACACCTGNTCCTCCAGGCAGCTGTCCAGGGCGCCAGGCCTGCCCTGCACCACAGCCCTCAGGAAATCCGGCA
AGGAGGGCCCTGCAGGTGGTTCAGCCAGGTAGCAAAACAGACACAGCAGCCCGCCTGACCCCTGCCCCNT
CTGTGGAGGCCCCGGGACCCCGCAATAAGCACCACATGGGTGAGGCTGTCCCTGTGAGGNCCTGCCAGGGTCCCTC
CTGGGGTCTGGGCCATTTGAGGGGCTCTTGATGGGCCAGGCCGCCAGAGTGAATCCGAGCACTTTCTGGCTGGT

FIG. 1C

*->vAvKilkklesls....lrEiqilkrIs.HpNIvrllyvfedtdhly [SEQ ID NO:7]
+A+K ++k+++ ++ lrE++i ++ls+ p+I++++v+ +t+d +
32374 1 MALKFVNKSKTKlknfLREVSITNSLSsSPFIKVFVDVVFETEDCYV 47

lvmEymegGdLfdylrrngplsekeakkialQilrGleYlHsngivHRDL
+ +Ey++ GdLfd++ + l+e+ +k+++ Q+ +l+++H++ vHRD+
32374 48 FAQEYAPAGDLFDIIPPQVGLPEDTVKRCVQQLGLALDFMHGRQLVHRDI 97

KpeNILlden..gtvKiaDFGLArll.eklTtfvGTpwYmmAPEvileg.
KpeN+Ll +++ vK+aDFG+ r ++ + + + GT++Y APEv + +
32374 98 KPENVLLFDRecRRVKLADFGMTRRVgCRVKRVSGTIPYT-APEV-CQAg 145

FIG. 3A

4/21

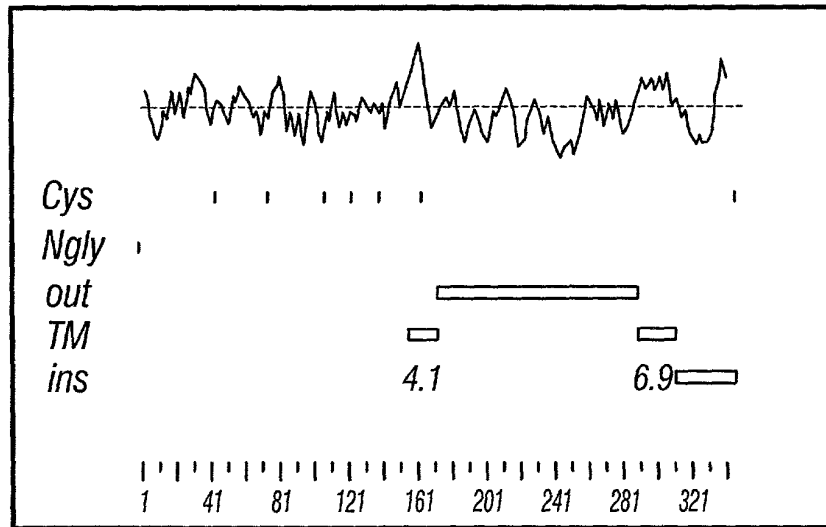


FIG. 2

5/21

```
....rgysskvDvWSlGviLyElItggplfpgadlpaftggdevdqliif
+ ++ ++ vDvW++Gv+++ +ltg
32374 146 radgLAVDVTGVDVWAFGVLFVCVLTG----- 171

vklkPfsdelpktridpleelfrikkr.....rlplpsncSeelkdL
P++ + ++ ++ ft r +++++ +++++ +++++ e+++
32374 172 --NFPWEAA-----SGADAFFEEFVRwqrgrlpgLPSQWRRFTEPALRM 213

lkkcLnkDPskRpGsatakei<-*
++L++ P++R ake+
32374 214 FQRLLEPERRG---PAKEV 231
```

FIG. 3B

```
Query: 226 GPAKEVFRFLKHELTSELRRRPSHRARKPPGDRPPAAGPLRLLEAPGPLKRTVLTESGSGS 285
          GPAKEVFRFLKHELTSELRRRPSHRARKPPGDR P GPLRLLEAPGPLKRTVLTESGSGS
Sbjct: 1 GPAKEVFRFLKHELTSELRRRPSHRARKPPGDRLP--GPLRLLEAPGPLKRTVLTESGSGS 58 [SEQ ID NO:8]

Query: 286 R 286
          R
Sbjct: 59 R 59
```

FIG. 4

```
Query: 321 PPGRTDGRADKSKGQVVLATAIEICV 346
          PPGRTDGRADKSKGQVVLATAIEICV
Sbjct: 89 PPGRTDGRADKSKGQVVLATAIEICV 114 [SEQ ID NO:9]
```

FIG. 5

```
Query: 166 FCVLTGNFPWEAASGADAFFEEFVRWQGRPLPGLPSQWRRFTEPALRMFQRLLEPERR 225
          +C + G FPW+ AS + E+ +W + + P LP ++ F+E AL++F++ L + R
Sbjct: 3 YC-MKGKFPWQKASIMCKPYWEWEQWLKRKNPALPKKFNPFSEKALKLFKKSLTPRFKDR 61 [SEQ ID NO:10]

Query: 226 GPAKEVFRFL-KHELTSELRR 245
          AK++ + L K +L ++R
Sbjct: 62 WTAKDMRKCLAKEKLLKSVKR 82
```

FIG. 6

6/21

Query: 4 K FVNKSKTKLKNFLREVSTNSLSSSPFIKVFDFVFETEDCYVFAQEYAPAGDLFDIIP 63
K V SK + + L E+ + L ++ F+I + + + Y+ +Y+ + + I
Sbjct: 16 KMVAFSKREERILLEIDLYKKLENNEFVIDLMAHIVDDITHYLLFDKYSQ--NFLEYIE 73 [SEQ ID NO:11]

Query: 64 P-QVGLPEDTVKRCVQQLGL--ALDFMHGRQLVHRDIKPENVLLFDRECRVKLADFG 118
++G D +K G+ A++ +HG + H DIK P N+L + +K+ DFG
Sbjct: 74 ELKIGGEVDELKHLKYFSGIVSAIEQLHGFEFAHLDIKPANIL---KSGDTIKMIDFG 128

FIG. 7

Query: 47 VFAQEYAPAGDLFDIIPPQVGLPEDTVKRCVQ-----QLGLALDFMH-----GRQ 91
+ A E+ P G L D +V +D+ + +Q Q+ AL ++H G++
Sbjct: 175 MIALEWLPGGTLADYFQFKVREKDDSERSPIQLKMLSIYQVSQALKYIHSQLEFGQE 234 [SEQ ID NO:12]

Query: 92 LVHRDIKPENVLLFDRECR--VKLADFGMTRRVGCRVKRVSGTIPYTAPEV-CQAGRAD 148
L H I NVL+ + + R+ VKL DFG +G + I Y PE+ C A R
Sbjct: 235 LTHGRIFTRNVLTPEDLRKCEVKLGDFG-DAPMGLEYS--TPIIAYMPPEILCCAERIP 291

Query: 149 GLAVDTGVDVWAFGLIF-CVLTGNFP 174
+ DVW FGV I+ C+ G P
Sbjct: 292 PHRPEN--DVWMFGVFIWECLTLGAQP 316

FIG. 8

Query: 77 VQQLGLALDFMHGRQLVHRDIKPENVLL---FDRECRVKLADFGMTR-----RVGCRVK 128
+ QL A ++H ++ RD+K +N+LL FD E ++ +ADFG +V
Sbjct: 319 IAQLEACTYLHKHKVAQRDMKSDNILLEDFDDEIPQLVVADEFGALACDNWQVDYESD 378 [SEQ ID NO:13]

Query: 129 RVS--GTIPYTAPEVCQAGRADGLAVDTGV-DVWAFGLIFCVLTGNFPWEAASGADAFF 185
VS G APE+ A + V+ + D WA G L + VLT + P+
Sbjct: 379 EVSLGGNAKTKAPEIATAVPGKNVKNFEMADTWAAGGLSYEVLTRSNPFYKLL----- 432

Query: 186 EEFVRWQGRPLPLSQ 202
+ +Q LP LPS+
Sbjct: 433 -DTATYQESLPALPSR 448

FIG. 9

7/21

Query: 68 LPEDTVKRCVQQLGLALDFMHGRQLVHRDIKPENVLLFDR--ECRRVKLADFGMTRRVGC 125
LP D ++ L A+DF+ G + HRDIKP+N+ + R R + L DF + G
Sbjct: 647 LPVDQLEAYGDYLFQAVDFLEGEGLVHRDIKPDNIIVRIRPNRTRELVLIDFSLA---GY 703 [SEQ ID NO:14]

Query: 126 RVKRV-SGTIPYTAPEVCQAGRADGLAVDTGVDVWAFGVLFVCVLTGNFP-WEAASGADA 183
K +GT Y P V R + D+ + +A V + + +G P W S
Sbjct: 704 PAKNTDACTDGYLDPFVDVITRG---SYDSHAERYAVAVTLHQMASGELPKWGDGSQLPR 760

Query: 184 FFEFVVRWQGRPLPSQWRRTFTEPALR-----MFQRLALEPERRGPAKEVFR--FLK 236
+ W P + ++ F +PA+R FQ+ L + +R P + R + K
Sbjct: 761 MTDK-KEWP---YPTIAAE--AF-DPAVRDGLVAFFQKALHRDACKRFPELPMRDWRK 813

Query: 237 HELTSELRRRPSHRARKP-PGD-RPPAAG 263
L + SHR R P D PA G
Sbjct: 814 VFLDASQTVPSHRTRPAAPADGAAPAEG 842

FIG. 10

Query: 30 PFIIKVFVDVVFETEDCYFAQYAPAGDLFDIIPPQVGLP----EDTVKRCVQQLGLALD 85
P I+ + +V E + C++ QE G + + G+P E+ + +QQL LD
Sbjct: 71 PGLAIENVSEEDRCFLVTQEND--GPILSLTQYLGIPRKLTEEEIVDIIQQLCSLLD 128 [SEQ ID NO:15]

Query: 86 FMHGRQLVHRDIKPENVLL-FDRECRVKLADFGMTRRVGCR-----VKRV 130
++H L H +V + F + L D G + R +++
Sbjct: 129 YVHSEGLAHGQWNLHSVHIHFLNGVPIYLPDLGFASLIRERMFDFMQDEENRESIEKI 188

Query: 131 SGTIPYTAPEVCQAGRADGLAVDTGVNVWAFGVLFVCVLTGNFPWEAASGADAFEEFV 189
+ + PE Q +G DT +AFG + + +L G FPW F +F+
Sbjct: 189 RDRLLFHTPEGRQT---NGRETDT---YAFGAITYYLLFGFFPWGIFPKPSKCFPDFI 240

FIG. 11

Query: 29 SPFIKVFVDVVFETEDC-YVFAQYAPAGDLFDIIPPQVGLPEDTVKRCVQQLGLALDFM 87
SP ++ V D++ E E VF E L +++ PE ++ L L
Sbjct: 82 SPHVLPRDIKPEGEWLSLVF--EPRRTITRELLSAGPVSP-LLQPLTTALFEGLSAA 138 [SEQ ID NO:16]

Query: 88 HGRQLVHRDIKPENVLLFDRECRVKLADFGMTRRVGCRVKSQGTIP-YTAPEVCQAGR 146
H L+H I PE V FD + +R LA+FG+ RR ++ P Y APE+ G
Sbjct: 139 HQGALLHTQISPEAVW-FDTQ-KRPLLAEEGLARRTAQELRDHWPDPYAAPELLSGG- 195

FIG. 12A

8/21

Query: 147 ADGLAVDTGVDVWAFGLIFCVLTGNFPWEAASGADAFEEFVRWQGRLP----GLPSQ 202

D++A + EAA+G A R Q RLP G+P Q

Sbjct: 196 ----PYTPQTDLYALAATLL-----EAATGT-ALSPVSARQQGVRLPSWPAGIPPQ 241

Query: 203 WRRFTEPALRMFORLLALEPERRGPAKEVFRFLKH-ELTSELRRRPSHRARKPPGDRPPA 261

E L++ +A+ A EV L+ +T + + A P PPA

Sbjct: 242 VAHALESCLQLDPAVRAVS-----AAEVLEELRRAQPTQAILSQQEPPAPPPSVPSPPA 295

Query: 262 A 262

A

Sbjct: 296 A 296

FIG. 12B

CTTCCTCTTCCTGTGCTCAGTCCCATTAACTGCCATACCACGGCTCCTCGTCTTCCCAATTCCTCACCAGTATTTT [SEQ ID NO:4]

CAATCGACCCCCCGTCCCCCGCACCTCTTTCTCTCGCTATATGTCCTTTCGTGGCCAGTTTGGGCAAGGGGAA

GGACACCACAAGTCGGGGTCTTTCTCAGCGTTGGGTCGGGTGGCTGTGAGGGCGGAAGAAAAGGCCAGGCTGAGGGG

AGGGTAGAGGGTGAAGAGCTCGGATCTGTGTTTGGGGAAGGCCAGGCTTGGCTCCTCGCCGGGTTCGCGAAGGTAA

CCTTGGCTGACTTGGCTCGCGAGCAAAGGGCAGCCTCTGAGCTCCCGCGTTCAGGAGTGGCTCTTTTGTAGGAGCA

CCTGAAATGCAGCTCTGGTGCCTAAGCCGTAGCGGCAGCAGCCAGCGACAGCGCTGGGGCCCTGTGTAGAAG

CTCCATCCCCCTTGTCTTTGTGCTTGCCTGCGTCCCCAGACTCAGAGATTATCTTAGAAGACCTAGGACTCCAAA

M F P L K D A E M G A F T F F A S A L P 20 [SEQ ID NO:5]

ATG TTT CCC CTG AAG GAC GCT GAA ATG GGA GCC TTT ACC TTC TTT GCC TCG GCT CTG CCA 60

↑SEQ ID NO:6 →

H D V C G S N G L P L T P N S I K I L G 40

CAT GAT GTT TGT GGA AGC AAT GGA CTT CCT CTC ACA CCA AAT TCC ATC AAA ATT TTA GGG 120

R F Q I L K T I T H P R L C Q Y V D I S 60

CGC TTT CAA ATC CTT AAA ACC ATC ACC CAT CCC AGA CTC TGC CAG TAT GTG GAT ATT TCT 180

R G K H E R L V V V A E H C E R S L E D 80

AGG GGA AAG CAT GAA CGA CTA GTG GTC GTG GCT GAA CAT TGT GAA CCT AGT CTG GAA GAC 240

FIG. 13A

9/21

L L R E R K P V S C S T V L C I A F E V 100
TTG CTT CGA GAA AGG AAA CCT GTG AGC TGT TCA ACG GTT TTG TGT ATA GCA TTT GAG GTT 300

L Q G L Q Y M N K H G I V H R A L S P H 120
CTT CAG GGC TTG CAG TAT ATG AAC AAA CAT GGT ATA GTA CAC AGG GCA TTG TCT CCT CAT 360

N I L L D R K G H I K L A K F G L Y H M 140
AAT ATC CTG TTG GAC CGA AAG GGA CAT ATT AAA TTG GCT AAA TTT GGA CTT TAT CAC ATG 420

T A H G D D V D F P I G Y P S Y L A P E 160
ACA GCT CAT GGT GAT GAT GTT GAT TTC CCA ATA GGG TAT CCC TCG TAC TTG GCC CCT GAG 480

V I A Q G I F K T T D H M P S K K P L P 180
GTA ATT GCA CAG GGA ATT TTC AAA ACC ACT GAT CAC ATG CCA AGT AAA AAA CCA TTG CCT 540

S G P K S D V W S L G I I L F E L C V G 200
TCT GGC CCC AAA TCA GAT GTA TGG TCT CTT GGA ATC ATT TTA TTT GAG CTT TGT GTG GGA 600

R K L F Q S L D I S E R L K F L L T L D 220
AGA AAA TTA TTT CAG AGC TTG GAT ATT TCT GAA AGA CTA AAA TTT TTG CTT ACT TTG GAT 660

C V D D T L I V L A E E H G C L D I I K 240
TGT GTA GAT GAC ACT TTA ATA GTT CTG GCT GAA GAG CAT GGT TGT TTG GAC ATT ATA AAG 720

E L P E T V I D L L N K C L T F H P S K 260
GAG CTT CCT GAA ACT GTG ATA GAT CTT TTG AAT AAG TGC CTT ACC TTC CAT CCT TCT AAG 780

R P T P D E L M K D K V F S E V S P L Y 280
AGG CCA ACC CCA GAT GAA TTA ATG AAG GAC AAA GTA TTC AGT GAG GTA TCA CCT TTA TAT 840

T P F T K P A S L F S S S L R C A D L T 300
ACC CCC TTT ACC AAA CCT GCC AGT CTG TTT TCA TCT TCT CTG AGA TGT GCT GAT TTA ACT 900

L P E D I S Q L C K D I N N D Y L A E R 320
CTG CCT GAG GAT ATC AGT CAG TTG TGT AAA GAT ATA AAT AAT GAT TAC CTG GCA GAA AGA 960

S I E E V Y Y L W C L A G G D L E K E L 340
TCT ATT GAA GAA GTG TAT TAC CTT TGG TGT TTG GCT GGA GGT GAC TTG GAG AAA GAG CTT 1020

V N K E I I R S K P P I C T L P N F L F 360
GTC AAC AAG GAA ATC ATT CGA TCC AAA CCA CCT ATC TGC ACA CTC CCC AAT TTT CTC TTT 1080

FIG. 13B

10/21

E D G E S F G Q G R D R S S L L D D T T 380
GAG GAT GGT GAA AGC TTT GGA CAA GGT CGA GAT AGA AGC TCG CTT TTA GAT GAT ACC ACT 1140

V T L S L C Q L R N R L K D V G G E A F 400
GTG ACA TTG TCG TTA TGC CAG CTA AGA AAT AGA TTG AAA GAT GTT GGT GGA GAA GCA TTT 1200

Y P L L E D D Q S N L P H S N S N N E L 420
TAC CCA TTA CTT GAA GAT GAC CAG TCT AAT TTA CCT CAT TCA AAC AGC AAT AAT GAG TTG 1260

S A A A T L P L I I R E K D T E Y Q L N 440
TCT GCA GCT GCC ACG CTC CCT TTA ATC ATC AGA GAG AAG GAT ACA GAG TAC CAA CTA AAT 1320

R I I L F D R L L K A Y P Y K K N Q I W 460
AGA ATT ATT CTC TTC GAC AGG CTG CTA AAG GCT TAT CCA TAT AAA AAC CAA ATC TGG 1380

K E A R V D I P P L M R G L T W A A L L 480
AAA GAA GCA AGA GTT GAC ATT CCT CCT CTT ATG AGA GGT TTA ACC TGG GCT GCT CTT CTG 1440

G V E G A I H A K Y D A I D K D T P I P 500
GGA GTT GAG GGA GCT ATT CAT GCC AAG TAC GAT GCA ATT GAT AAA GAC ACT CCA ATT CCT 1500

T D R Q I E V D I P R C H Q Y D E L L S 520
ACA GAT AGA CAA ATT GAA GTG GAT ATT CCT CGC TGT CAT CAG TAC GAT GAA CTG TTA TCA 1560

S P E G H A K F R R V L K A W V V S H P 540
TCA CCA GAA GGT CAT GCA AAA TTT AGG CGT GTA TTA AAA GCC TGG GTA GTG TCT CAT CCT 1620

D L V Y W Q G L D S L C A P F L Y L N F 560
GAT CTT GTG TAT TGG CAA GGT CTT GAC TCA CTT TGT GCT CCA TTC CTA TAT CTA AAC TTC 1680

N N E A L A Y A C M S A F I P K Y L Y N 580
AAT AAT GAA GCC TTG GCT TAT GCA TGT ATG TCT GCT TTT ATT CCC AAA TAC CTG TAT AAC 1740

F F L K D N S H V I Q E Y L T V F S Q M 600
TTC TTC TTA AAA GAC AAC TCA CAT GTA ATA CAA GAG TAT CTG ACT GTC TTC TCT CAG ATG 1800

I A F H D P F L S N H L N E I G F I P D 620
ATT GCA TTT CAT GAT CCA GAG CTG AGT AAT CAT CTC AAT GAG ATT GGT TTC ATT CCA GAT 1860

L Y A I P W F L T M F T H V F P L H K I 640
CTC TAT GCC ATC CCT TGG TTT CTT ACC ATG TTT ACT CAT GTA TTT CCA CTA CAC AAA ATT 1920

FIG. 13C

11/21

F H L W D T L L L G N S S F P F C I G V 660
TTC CAC CTC TGG GAT ACC TTA CTA CTT GGG AAT TCC TCT TTC CCA TTC TGT ATT GGA GTA 1980

A I L Q Q L R D R L L A N G F N E C I L 680
GCA ATT CTT CAG CAG CTG CGG GAC CGG CTT TTG GCT AAT GGC TTT AAT GAG TGT ATT CTT 2040

L F S D L P E I D I E R C V R E S I N L 700
CTC TTC TCC GAT TTA CCA GAA ATT GAC ATT GAA CGC TGT GTG AGA GAA TCT ATC AAC CTG 2100

F C W T P K S A T Y R Q H A Q P P K P S 720
TTT TGT TGG ACT CCT AAA AGT GCT ACT TAC AGA CAG CAT GCT CAA CCT CCA AAG CCA TCT 2160

S D S S G G R S S A P Y F S A E C P D P 740
TCT GAC AGC AGT GGA GGC AGA AGT TCG GCA CCT TAT TTC TCT GCT GAG TGT CCA GAT CCT 2220

P K T D L S R E S I P L N D L K S E V S 760
CCA AAG ACA GAT CTG TCA AGA GAA TCC ATC CCA TTA AAT GAC CTG AAG TCA GAA GTA TCA 2280

P R I S A E D L I D L C E L T V T G H F 780
CCA CGG ATT TCA GCA GAG GAC CTG ATT GAC TTG TGT GAG CTC ACA GTG ACA GGC CAC TTC 2340

K T P S K K T K S S K P K L L V V D I R 800
AAA ACA CCC AGC AAG AAA ACA AAG TCC AGT AAA CCA AAG CTC CTG GTG GTT GAC ATC CGG 2400

N S E D F I R G H I S G S I N I P F S A 820
AAT AGT GAA GAC TTT ATT CGT GGT CAC ATT TCA GGA AGC ATC AAC ATT CCA TCC AGT GCT 2460

A F T A E G E L T Q G P Y T A M L Q N F 840
GCC TTC ACT GCA GAA GGG GAG CTT ACC CAG GGC CCT TAC ACT GCT ATG CTC CAG AAC TTC 2520

K G K V I V I V G H V A K H T A E F A A 860
AAA GGG AAG GTC ATT GTC ATC GTG GGG CAT GTG GCA AAA CAC ACA GCT GAG TTT GCA GCT 2580

H L V K M K Y P R I C I L D G G I N K I 880
CAC CTT GTG AAG ATG AAA TAT CCA AGA ATC TGT ATT CTA GAT GGT GGC ATT AAT AAA ATA 2640

K P T G L L T I P S P Q I * 894
AAG CCA ACA GGC CTC CTC ACC ATC CCA TCT CCT CAA ATA TGA 2682

← SEQ ID NO:6↑

AGAACCAAGAGTGTGACTGCCAAAACCTAGTGTGGCATCAGCACCAACAGCACAGTTCTTCATATCCACGCCACTCTCA

FIG. 13D

12/21

GACAAACTAGATGTCCAGATTGTTGCATTTCCGTAAGTTTGTACGAGACATTTTTTAAATCTCATAACCCACATG
TTCAGTTATCCATGCCAAGAACTTGACTCTACATGTATTGCTGAAAGAATTTCTTAACAGTGAAATCTGATCATATAT
TTTTACCACACTGCCACATAAGCCCAAGAAATTCAGCTGACAAGACAGATTTAGCATTATCAAGAAATCNNATTGCC
CTGAAAAGCTGTCTCCATTGTAAGACAGACAGTCTGTCGATTGTGTTATTAGAAACATACACTGAATGTGGGC
TGAAATCATCATTTTCCATAATGAAAAGTGAAGAACTATTCACAATGCATTCTTATAAATAAATGCTACATTAGTA
ACTCATTTACCCAAACAAGAGATGTGTGTGTGTGTGTATAGGAAGTGGAGTTATCCCATTCAGAAACTGTN
AATACTTACTCCAGAAAAATGAAATTTAGAAACCATTATATTGATAGAATATTGGTCAGTTCCTGTAGCAAAGAC
GAATGGCTTAAACAAATTTCTAGTTCTTTATCAGTGAAGTCTGTACAGTCAGTCCAGGGCTAGTCTACTGCTTTC
CTGATCATTAAGAACTATTACCTTCTCTCATTTGCTTTACAAACCTCAATATGTGGCATCCATCTCATGGATGAAATG
GCTCCTCAGCTTCTACCATCACATCTGCTATCTAGAAGGAAGAGAATGAGGGAAGGAGGGAGGGGATGAAGAGAAAAGA
AGGAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 13E

13/21

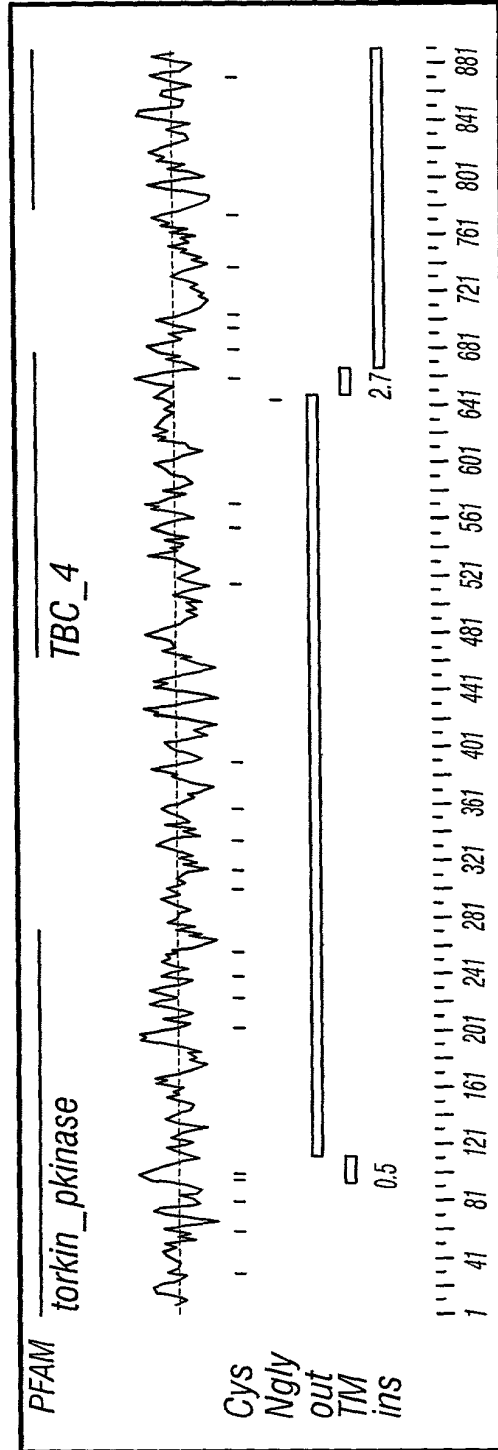


FIG. 14

14/21

*->qilkrIsHpNIvrllgvfedtdhhlylvmEymegGdLfdylrrngpl [SEQ ID NO:17]
qilk++ Hp ++++ ++ + +++l +v E++e +L d+lr+++p
18431 43 QILKTITHPRLCQYVDISRGKHERLVVVAEHCER-SLEDLLRERKPV 88

sekeakkialQilrGleYlHsngivHRDLKpeNILldengtvKiaDFGLA
s +++ia ++l+Gl+Y+ +givHR L p NILld++g++K+a FGL
18431 89 SCSTVLCIAFEVLQGLQYMNKHGIVHRALSPHNILLDRKGHIKLAFLGLY 138

rll...eklttfvGTPwYmmAPEvi.....leg.rgysskvDv
++ G p Y APEvi ++ +++++ + + + ++k+Dv
18431 139 HMTahgDDVDFPIGYPSYL-APEVIaaggifktt dhmpSKKpLPSGPKSDV 187

WSlGviLyElltggplfpgadlpafthggdevdqliifvklpfsdelpkt
WSlG+iL+El+ g++lf+++d ++ 1 +
18431 188 WSLGIILFELCVGRKLFQSLD-----ISERLKFLLTL 219

ridpleelfrikkr.rlpplsncSeelkdLlkkcLnkDPskRpGsatake
++ ++ +++ l++ ++++e+++dLl+kcL++ PskRp t e
18431 220 DCVDDTLIVLAAEHgCLDIKELPETVIDLLNKCLTFHPSKRP---TPDE 266

ilnhpwf<-*
+++++ f
18431 267 LMKDKVF 273

FIG. 15

15/21

```

*->vrqgvpslRgkVWklIlIgaqelnncIltdnfkgldlfglvpvllla [SEQ ID NO:18]
      r +p +Rg W++llg      +
18431  463  ARVDIPPLMRGLTWAALLGVEGAI----- 486

      dkdeYeellnknkektvqdqneKssvgirrldyVEAVEKHPLSDDNDKTK
      Y++++ ++ +t
18431  487 -HAKYDAIDKDTPIPT----- 501

      GSLekgsdekalklredldkIekDlsRTfpdeiffqtrlaeqqlkdkdql
      + +Ie D+ R+ + +++
18431  502 -----DRQIEVDIPRCHQYDELL----- 519

      daydkDEfddeddkneppsikqLrrlLvaYswknpqehlgYvQGMnvils
      +p++++ rr+L a ++ +p+ l Y QG ++
18431  520 -----SSPEGHAKFRRVLKAWVVSHPD--LVYWQGLDSLCA 553

      pLLlf.lkhgvdldedeegAFwclvkLmdnylpqkyflndls.glnedl
      p+L+++      +e A++c +++ +yl + +fl+d st ++e l
18431  554 PFLYLnFN-----NEALAYACMSAFIPKYLYN-FFLKDNShVlQEYL 594

      rvLdslvkeslPeLyshlkkkenktgsgkKknllaldltllifafpwlLt
      v++ + + +PeL++hl+      + +++++a+pwlLt
18431  595 TVFSQMIAFHDPELSNHLNEI-----GFIPDLYAIPWFLT 629

      lFarelPleivlrIwDilftyYlgshflifvalAiLklklsklkh<-*
      F+ ++Pl ++++wD l++ +s+f++ ++AiL++l++ ll+
18431  630 MFTHVFPLHKIFHLWDTLILG--NSSFPFCIGVAILQQLRDRLAN 673

```

FIG. 16

16/21

Query: 459 IWKEARVDIPPLMRGLTWAALLGVEGAHAKYDAIDKDT-----PIPTDRQIEVDIPRC 512
I +E +D+PP +RG W LL V + +Y +D P P DRQ+EVDIPRC
Sbjct: 1 IQRETNIDVPPTLRGEVWGCLLRVPPSARTRYALLDHAVHHTAAKPTPHDRQLEVDIPRC 60 [SEQ ID NO:19]

Query: 513 HQYDELLSSPEGHAKFRVLKAWVVS--PDLVYNQGLDSLCAFFLYLNFNNEALAYACM 570
HQY LL+SP G A+ RR+LKAW + + P+ VYWNQGLDSLCAFFL +N +EALA+A +
Sbjct: 61 HQYHPLLNSPSGSAQLRRILKAWQIVYLRPEHVYWNQGLDSLCAFFLTVNNRDEALAFAL 120

Query: 571 SAFIPKYLNFELKDNSHVIQEYLTVESQMIAFHDPESNLHNEIGFIPD 620
+AF+ +Y++ F+LKDNS VI+EYL F + A+HDP L HL GF P+
Sbjct: 121 NAFVNRYIHWFYLDNSSEVIKEYLGRFYHLTAYHDPLLYQHLKINGFDPE 170

FIG. 17

Query: 27 NGLPLTPNSIKILGRFQILKTITHPRLCQYVDISRGKHER--LVVVAEHCSLEDLLRE 84
NGLPLTP + ++LGRF L+ + H LCQY+ RGKHER +VV EH +LED +
Sbjct: 1 NGLPLTPPAKQMLGRFPYLOELQHDHLCQYLHFIRGKHERDLTIVVMEHYGMNLEDYAKR 60 [SEQ ID NO:20]

Query: 85 RKPVSCSTVLCIAFEVLQGLQYMNKHGIVHRALSPHNILL----DRKGHIKLAKFGLYHM 140
P + +++ G+ Y+++H IVH L P++I + +RK +KL +GL+HM
Sbjct: 61 HPPKDEAQNNNFYQIACGINYLHRHHIVHHNLHPNHIYITDDGNRKL SVKLFNYGLHMH 120

Query: 141 TAHGDDVDFPOGYPSYLAPEVIAQGIFKTTDHMXXXXXXXXXXXXVWSLGIILFELCVG 200
T +G FPIG Y+APE I D++ DVW LG I+ ++ +G
Sbjct: 121 TNYGKYTPFPIGNRYMAPE----RILNDNDNLFAATYQS-----DVWELGFIMLQIYLG 171

Query: 201 RKL 203
+L
Sbjct: 172 IEL 174

FIG. 18

17/21

Query: 322 IEEVYYLWCLAGGDLEKELVNKEIIRSKPPICTLPNFLFEDGESFGQGRXXXXXXXXXX 381
+ ++Y+LW LAGGD++ EL + +IRS+ PI LP + G S GR
Sbjct: 100 LSQIYHLWQLAGGDVQAEKKKEGLIRSEAPILGLPQIVRLSGASVCGRSQQLMDDRVR 159 [SEQ ID NO:21]

Query: 382 XXXXCQLNRNLKDVGGGEAFYPLEDDQSNLPHSNSNNELSAAATLPLIIREKDTEYQLNR 441
L RL + ++PLL + P ++ EL LPL+IREKD EYQ R
Sbjct: 160 PLRLKALLQRLSGLPAAVYFPLLHSPR--FP-AHFARELQE---LPLVIREKDIEYQFQR 213

Query: 442 IILFDRLLKAYPYKKNQ 458
+ LF RLL+ YP+ Q
Sbjct: 214 VRLFARLLQGYPHTAEQ 230

FIG. 19

Query: 207 LDISERLKFLTLDCVDDTLIVLAEHGCCLDIKELPETVIDLLNKCLTFHPSKRPTPDE 266
L +S ++ +L + L +A EH C + + + + LL CL+ P +RP P E
Sbjct: 4 LKLSNVVRKILAFGKSNGALEXIAREHQCHERYVQMDQRLRQLLESCLSVLPKRRPLPGE 63 [SEQ ID NO:22]

Query: 267 LMKDKVFSEV 276
L++ +F EV
Sbjct: 64 LLEHPIFEEV 73

FIG. 20

Query: 636 PLHKIFHLW 644
PL +I+HLW
Sbjct: 99 PLSQIYHLW 107 [SEQ ID NO 23]

FIG. 21

18/21

Query: 621 LYAIPWFLTMFTHVFPLHKIFHLWDTLTLLGNSFPFCIGVAILQQLRDRLL-ANGFNECI 679
LYA WFLT+F PL + +WD S F + +A+L+ ++ LL A+ F E +
Sbjct: 1 LYAFQWFLTLFARELPLETVLRIWDCCFFYEGSKILFRVALALLKMHKEELLQADDFEEML 60 [SEQ ID NO:24]

Query: 680 -LLFSDLP-----EIDIERCVRESINL 700
L + LP E D R + E+ N+
Sbjct: 61 EFLQNMLPKRYRSEEDARRLLEEACNI 87

FIG. 22

Query: 72 EHCERSLEDLLRERKPVSCSTV---LCIAFEVLQGLQYM----NKHGIVHRALSPHNILL 124
E E+ + + E+K S V + IA+++ +GL+Y+ NK I+HR L P NILL
Sbjct: 136 EMMEKLQKQSMSEKKMEEMSWVSQLMKIAYQIAKGLEYLHSSKNKQNIHRDLKPENILL 195 [SEQ ID NO:25]

Query: 125 DR----KGH-----IKLAKFGLYHM 140
D KG +K+A FGL M
Sbjct: 196 DNNMVAKGDSEIKVVKIADFGGLARM 220

FIG. 23

Query: 152 GYPSYLAPEVIAQGIFKTTDHMXXXXXXXXXXXXVWSLGIILFELCVGRKLF--QSLDI 209
G PSY+ ++ + ++ DVWS G+IL+EL G+ F S ++
Sbjct: 245 GTPSYV--KYVGTRWYMAPEVLMGSSYGQYSEKSDVWSFGVILYELLTGKPPFPFGSSEV 302 [SEQ ID NO:26]

Query: 210 SE-RLKFLTLDCVDDTLIVLAEHGCGLDIIKE---LP---ETVIDLLNKCLTFHPSKR 261
++ ++ ++ V + + + KE P E V DL+ KC P KR
Sbjct: 303 NDSQMNEIMKETMVKSAEYEMPMKMPPESSKESMSCPSMSSEAVKDLIKWCQKDPEKR 362

Query: 262 PTPDELMKDKVFSEV 276
PT +++++ E+
Sbjct: 363 PTFAQVVEELSAHEI 377

FIG. 24

19/21

Query: 740 PPKT-DLSRESIPLNDLKSEVSPRISAEDLIDLCELTVTGHFXXXXXXXXXXXXLLVVD 798
PP+ D+ + L L+ E PRISA+D+ L + L ++D
Sbjct: 29 PPQALDIGVADVELKHLQOEQCPRISAKDVQFLD-----NSPAELALID 73 [SEQ ID NO:27]

Query: 799 IRNSED FIRGHISGSINIPFSAFTAEGELTQGPYTAMLQNFKGKVVIVGVHAKHTAEF 858
+R+ +F R H+ SINIPF+ E L + +GK++V V ++ +H+ E
Sbjct: 74 LRSVVEFGRVHVPHSINIPFATVQLGEQRLQVPLEAQLRGKIVVCVSNHQHSVEV 133

Query: 859 AAHLVKMK 866
L ++K
Sbjct: 134 GHPLAQLK 141

FIG. 25

Query: 693 CVRESINLCWTPKSATYRQHA---QPPKXXXXXXXXXXAPYFSAECPDPPKTDL---- 745
CV ES ++ TPKS T+RQHA QPP+ +CP D+
Sbjct: 3 CVLESQKMYEATPKSITHRQHALRLOPPQALDIGVADVELKHLQOEQCPRISAKDVQFL 62 [SEQ ID NO:28]

Query: 746 --SRESIPLNDLKSEVS-PRISAEDLIDLCELTV 776
S + L DL+S V R+ I++ TV
Sbjct: 63 DNSPAELALIDLRSVVEFGRVHVPHSINIPFATV 96

FIG. 26

Query: 856 AEFAAHLVKMKYPRICILDGGIN---KIKPTGLLT 887
++F+ LV R CIL G N I+P L++
Sbjct: 152 SQFSHFLVACGVQRTCILHKGFNVLHSIEPNILIS 186 [SEQ ID NO:29]

FIG. 27

20/21

Query: 506 EVDIPRCHQYDELLSSPEGHAKFRVLKAWVVSHPD--LVYWQGLDSLCAFLYLNFNNE 563
+ DI C +Y+ P + + + L + + V +P + + + G APF YL
Sbjct: 336 DTDIGGCCFEYNTF-PPPGKYRGKLGLEEYAVFYPPNGVIPFHGFCMYAAPFCYLYHEPS 394 [SEQ ID NO:30]

Query: 564 ALAYACMSAFIPKYLYNFFLKDNSHV--IQEYLTVFSQMIAFHDPELSNHLNEIGFIPDL 621
L Y +I +Y + N+H I +F + + + +P+L H EIG P
Sbjct: 395 KLYYTFREFYI-RYCHRLHTI-NTHPQGIVSLCLLFEKLLQTYEPQLWYHFREIGAQPLR 452

Query: 622 YAIPWFLTMFTHVFLHKIFHLWDTLILGNS 652
+ W + F+ P ++ LWD +L NS
Sbjct: 453 ISFKWMMRAFSGHLPPDQLLLLDWRILGYN 483

FIG. 28

Query: 77 SLEDLLRERKPVSCSTVLC--IAFEVLQGLQYMNKHGIVHRALSPHNILLDRKGHIKLA 134
S LLR P S L I F ++GL Y+++G +HR++ +IL+ G + L+
Sbjct: 5 SASQLLRITYFPEGMSSETLIRNIFGAVRGLNYLHQNGCIHRSHIKASHILISGDGLVTL 64 [SEQ ID NO:31]

Query: 135 FG-LYHMTAHGDD----VDFP---IGYPSYLAPEVIAQGFKTTDHMXXXXXXXXXXXXD 186
L + + HG DFP +L+PE++ Q + H D
Sbjct: 65 LSHLSLVKHGQRHRAVYDFPQFSTSVQPWLSPELLRQDL-----H-----GYNVKS 112

Query: 187 VWSLGIILFELCVGRKLFQSLDISERL 213
++S+GI EL G+ FQ + ++ L
Sbjct: 113 IYSGITACELASGQVPFQDMHRTQML 139

FIG. 29

Query: 240 KELPETVIDLLNKCLTFHPSKRPTPELMKDKVFSEV 276
K L+ CL P KRP+ L+ F ++
Sbjct: 198 KTFSPAFFSLVQLCLQQDPEKRPSASSLLSHVFFKQM 234 [SEQ ID NO:32]

FIG. 30

21/21

Query: 596 VFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFELTMFTHVFPLHKIFHLWDTLILGNSSFP 655
+F ++ +HDPEL NHL+ PD+Y + WF ++F LWD + F
Sbjct: 18 LFRLLQYHDPELCNHLDTKKCTPDMYTLNWFGLFASCCSTEVCHALWDLYIQQADPFM 77 [SEQ ID NO:33]

Query: 656 -FCIGVAILQQLRDRL---ANGFNECILLFSDLP-EIDIE 691
F + + IL ++ +L ++ E I ++P +++IE
Sbjct: 78 VFFLALIILINAKKEIILQMKSDSKEEVIKFLENMPCQLNIE 118

FIG. 31

Query: 796 VVDIRNSED FIRGHISGSINI 816
+VD R +E + GH+S + ++
Sbjct: 194 IVD CRPAEQYNAGHLSTAFHL 214 [SEQ ID NO:34]

FIG. 32

Query: 112 IVHRALSPHNILLDRKGHIKLAFLYHMTAHGDDVD--FPIGYP--SYLAPEVIAQGIF 167
++HR + P +IL+ ++G KLA F + +D + FP Y + P + +
Sbjct: 1 VIHRNICPESILITKRGSWKLAGFDFCVSAQNPNQENYFPCHYEWDPRIPPLPLQPNLD 60 [SEQ ID NO:35]

Query: 168 KTTDHMXXXXXXXXXXXXVWSLGIILFELCVGRKLFQSLDISERLKFLLTLDCVDDTLI 227
D++SLG +++ + G K +D + ++ + +TL
Sbjct: 61 YLAPEYVTSSTCTVGSASDMFSLGCLIIAYNGGKPL--IDANNNDEYKSNYNKYMNTLN 118

Query: 228 VLAEEHGCLDIKELPETVIDLLNKCLTFHPSKRPTDELMDKVF 273
L H ++ + PE + + L + L+ P+ RPT EL K F
Sbjct: 119 SLT--HESMNNLP--PENLKESLKRMLSDPTVRPTAQELTLIKYF 160

FIG. 33

Query: 744 DLSRESIPLNDLKSEVSPRI--SAEDL-IDLCE 773
DL + P D+KS + P + + ED I +C+
Sbjct: 273 DLLLQKTPPEDIKSNILPMLYAFEDSDIQICQ 305 [SEQ ID NO: 36]

FIG. 34